

*Draft*

## RAW SEQUENCE LISTING ERROR REPORT

*L. Casper off*

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/236,995A  
Source: 1638  
Date Processed by STIC: 11/1/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE  
APPLICANT, WITH A NOTICE TO COMPLY or,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A  
NOTICE TO COMPLY  
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/236,99SA

## ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1  Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

2  Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

3  Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4  Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5  Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6  Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7  PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8  Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9  Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

10  Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11  Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.

12  Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13  PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

O:Haghmouj

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US-09/236,995A DATE: 11/01/2000  
TIME: 13:18:34

Input Set : A:\Polyadpl.app  
Output Set: N:\CRF3\11012000\I236995A.raw

3 <110> APPLICANT: Mahajan, Pramod B.  
4 Zuo, Zhuang  
6 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and Its Uses  
8 <130> FILE REFERENCE: 5718-34, 035718-174234  
10 <140> CURRENT APPLICATION NUMBER: 09/236,995A  
11 <141> CURRENT FILING DATE: 1999-01-26  
13 <150> PRIOR APPLICATION NUMBER: 60/072,785  
14 <151> PRIOR FILING DATE: 1998-01-27  
16 <160> NUMBER OF SEQ ID NOS: 5  
18 <170> SOFTWARE: PatentIn Ver. 2.1  
20 <210> SEQ ID NO: 1  
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22 <212> TYPE: DNA  
23 <213> ORGANISM: Zea mays  
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26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (1)..(2949)  
29 <220> FEATURE:  
30 <221> NAME/KEY: misc\_feature  
31 <222> LOCATION: ()..()  
32 <223> OTHER INFORMATION: n/a, T, C, or G  
34 <220> FEATURE:  
35 <221> NAME/KEY: misc\_feature  
36 <222> LOCATION: (1)..(2949)  
37 <223> OTHER INFORMATION: Xaa-unknown  
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41 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly  
42 1 5 10 15  
43 cng gec teg tgc aag tca tgc cgg tcc ect ate qcc aam gac caq ctc 96  
44 cng gec teg tgc aag tca tgc cgg tcc ect ate qcc aam gac caq ctc 101  
45 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu  
46 20 25 30  
47 cgt ctt qgc aag atg qtl cag qeq tca cag ttc qac qeq ttc arg ccc 144  
48 cgt ctt qgc aag atg qtl cag qeq tca cag ttc qac qeq ttc arg ccc  
49 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro  
50 35 40 45  
51 ccc 50 55 60  
52 atg tgg aac cat qcc aac agg tcc alc ttc aqc aag aac aac ala aaa 192  
53 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys  
54 50 55 60  
55 tcc gtt qac dat qtt qaa qqt ala dat qea ctt aqa tgg dat qst cca 240  
56 tcc gtt qac dat qtt qaa qqt ala dat qea ctt aqa tgg dat qst cca  
57 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln  
58 65 70 75 80  
59 gac aag ala ega aac ttc qtt qaa qqt qee tca get qst aca aqt tct 288  
60 gac aag ala ega aac ttc qtt qaa qqt qee tca get qst aca aqt tct  
61 Glu Lys Ile Arg Asn Tyr Val Glu Ser Ala Ser Ala Glu Thr Ser Ser  
62 85 90 95  
63 aca get get get ect qag aac ttc aac aac qpp att get cca tct qcc 336  
64 aca get get get ect qag aac ttc aac aac qpp att get cca tct qcc  
65 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala  
66 100 105 110

Does Not Comply  
Corrected Diskette Needed

slip 6/9  
PF

## RAW SEQUENCE LISTING

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DATE: 11/01/2000

TIME: 13:18:34

Input Set : A:\Polyadpl.app

Output Set: N:\CRF3\11012000\I236995A.raw

68	cgt	act	tca	tgt	aga	cga	tgc	agt	gaa	aug	att	aca	aaa	gga	tcg	gtc		384		
69	Arg	-Thr	Ser	Cys	Arg	Arg	Cys	Ser	Glu	Lys	Ile	Thr	Lys	Gly	Ser	Val				
70																	125			
71																		125		
72	cgt	ctt	tca	gtc	aag	ctt	gag	agt	gaa	ggg	ccc	aag	ggg	ata	cca	tgg		432		
73	Arg	Leu	Ser	Ala	Lys	Leu	Glu	Ser	Glu	Gly	Pro	Lys	Gly	Ile	Pro	Trp				
74																		140		
75																		140		
76	tat	cat	gcc	aac	tgt	ttc	ttt	gag	gtt	tcc	ccg	tct	gca	act	gtt	gag		480		
77	Tyr	His	Ala	Asn	Cys	Phe	Phe	Glu	Val	Ser	Pro	Ser	Ala	Thr	Val	Glu				
78	145																155	160		
79	aag	tcc	tca	ggc	tgg	gtt	act	tgt	ttc	gtt	gag	gtt	aag	aga	acc	atg		528		
80	Lys	Phe	Ser	Gly	Trp	Asp	Thr	Leu	Ser	Asp	Glu	Asp	Lys	Arg	Thr	Met				
81																	170	175		
82																	165	170		
83	ctc	gat	ctt	gtt	aaq	aat	gtt	ggc	aac	aat	gaa	caa	aat	aag	ggt			576		
84	Leu	Asp	Leu	Lys	Lys	Asp	Val	Gly	Asn	Asn	Glu	Gln	Asn	Lys	Gly					
85																	180	185	190	
86																		624		
87	tcc	aag	cgc	aaq																
88	Ser	Lys	Arg	Lys	Lys	Ser	Glu	Asn	Asp	Ile	Asp	Ser	Tyr	Lys	Ser	Ala				
89																	195	200	205	
90																		672		
91	agg	tta	gtt	qaa	agt	aca	tct	gaa	gtt	aca	gtt	cga	aac	aaa	ggg	caa				
92	Arg	Leu	Asp	Glu	Ser	Thr	Ser	Glu	Gly	Thr	Val	Arg	Asn	Lys	Gly	Gln				
93																	210	215	220	
94																		726		
95	cgt	gac	cca	cgt	tgt	tcc	aat	act	agt	tca	gtt	gtt	ata	caa	cta					
96	ctt	gtt	gac	cca	cgt	tgt	tcc	aat	act	agt	tca	gtt	gtt	ata	caa	cta				
97	Leu	Val	Asp	Pro	Arg	Gly	Ser	Asn	Thr	Ser	Ser	Ala	Asp	Ile	Gln	Leu				
98																	230	235	240	
99																		768		
100	aag	ctt	aaq	gaa	aaq															
101	Lys	Leu	Lys	Glu	Gln	Ser	Asp	Thr	Leu	Trp	Lys	Leu	Lys	Asp	Gly	Leu				
102																	245	250	255	
103	aag	act	cat	gtt	ttt	gtt		816												
104	Sys	Thr	His	Val	Ser	Ala	Ala	Glu	Leu	Arg	Asp	Met	Leu	Glu	Ala	Asn				
105																	260	265	270	
106																		864		
107	ggg	caq	gtt	aca	tca	ttt	gaa	ttt												
108	Gly	Gln	Asp	Thr	Ser	Gly	Pro	Glu	Arg	His	Leu	Leu	Asp	Arg	Cys	Ala				
109																	275	280	285	
110																		912		
111	gtt	gaa	atq	ctt	ttt	gaa														
112	Gly	Met	Tyr	Tyr	Tyr	Asn	Gly	Gln	Tyr	Gly	Ser	Cys	Ser	Gly	Asn	Val	Ser			
113	Asp	Gly	Met	Leu	Phe	Gly	Ala	Leu	Gly	Pro	Cys	Pro	Val	Cys	Ala	Asn		310	315	320
114																	290	305	300	
115																		960		
116	ggc	atg	tac	tat	tat	gtt														
117	Gly	Bet	Tyr	Tyr	Tyr	Asn	Gly	Gln	Tyr	Gly	Ser	Cys	Ser	Gly	Asn	Val	Ser			
118																	305	310	315	
119	aaq	tgg	tcc	aaq	tgt	aca	tac	tct	gtc	aca	gaa	cct	gtc	cgc	gtt	aag		1008		
120	Lys	Tyr	Asp	Leu	Asn	aaq	tgt	aca	tac	tct	gtc	aca	gaa	cct	gtc	cgc	gtt			
121	Glu	Trp	Ser	Lys	Cys	Thr	Tyr	Ser	Ala	Thr	Glu	Pro	Val	Arg	Val	Lys				
122																	325	330	335	
123	aag	aag	tgg	caa	att	cca	cat	qqa	aca	aaq	aat	gtt	tac	ctt	atq	aag		1056		
124	Lys	Lys	Trp	Gln	Met	Leu	Pro	His	Gly	Thr	Lys	Asn	Asp	Tyr	Leu	Met	Lys			
125																	355	360	365	
126																	310	345	350	
127	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt		1104		
128	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt				
129	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt				
130																	355	360	365	
131																		1152		
132	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt				

RAW SEQUENCE LISTING DATE: 11/01/2000  
 PATENT APPLICATION: US/09/236,995A TIME: 13:18:34

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133 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu		
134 370 375 380		1200
136 ctg tct tct aaa qgg ttg gat aaa tta agg ttt tct gtt gta gga caa		
137 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln		
138 385 390 395 400		1248
140 tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt		
141 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Ala Gly		
142 405 410 415		1296
144 qcc aac itc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca		
145 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala		
146 420 425 430		1344
148 tqt gat qaq ctc qac aat gaa aut gct gaa gtc agg aaa gca agg aag		
149 Cys Cty Glu Leu Asp Asn Glu Ala Glu Val Arg Lys Ala Arg Arg		
150 435 440 445		1392
152 ctg aag ata cca att cta agg qag ggt tac att gga gaa tqt gtt aaa		
153 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys		
154 450 455 460		1440
156 aqa aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta qag		
157 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu		
158 465 470 475 480		1488
160 trc tca aaa qgc mqt act gtc act gtt daa gtt aag qgc cqa agt act		
W--> 161 Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala		
162 485 490 495		1536
164 ttt Leu Tyr aqt ctc cyg gtt tgc aag dat act gct cac att cct tra		
W--> 165 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa		
166 500 505 510		1584
W--> 168 gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn		
W--> 169 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa		
170 515 520 525		1632
W--> 172 cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat		
W--> 173 His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp		
174 530 535 540		1686
175 dat qqq dat iaq tgc tac gta ttt cgt aag tgg gga cgg gtt qgg qgi		
177 Asp Cty Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gl Ser		
178 545 550 555 560		1728
180 qaa aua att qqa uqq csa daa ctc qag qag atg tca aaa act qaq qca		
181 Gln Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala		
182 565 570 575		1824
184 atc aag gaa ttc aai aqa tta ttt ctt gag aag act gga aac tca ttt		
185 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp		
186 580 585 590		1872
188 qaa qct tgg yaa tgg aat acc dat ttt cgg aag cag dat qgg aya ttt		
189 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro GLY Arg Phe		
190 595 600 605		1920
192 lac cca ctt qat gtt qat lat ggt gtt aag aaa gca cca aaa cgg aca		
193 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys		
194 610 615 620		
196 qat atc aqt qaa atq qaa qnt tct ctt gct cct cca ttg cta qaa ctc		
197 Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu		

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Input Set: A:\Polyadpl.app  
Output Set: N:\CRF3\11012000\I236995A.raw

198	625	630	635	640	1968
200	atg aag atg ctt ttt aat gtc gag aca tat aga gct gct atg atg gaa				
201	Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu				
202	645	650	655		2016
204	ttt gaa awt aat atg tca gaa atg cct ctt ggg uag cta agc mag gra				
W-->	205 Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa				
206	660	665	670		2064
208	aat att gag raa gga ttt gaa gca tta act krg rta cmq rat tta ttt				
W-->	209 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Leu Phe				
210	675	680	685		2112
W-->	212 gaa gga cac cgc tna tca agc act ggc ttg ttr gag aac gct naa ttg				
W-->	213 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu				
214	690	695	700		2160
216	ttt ytg sqa gem ats syt ttt tca ctc tta tcc ctr cta ttc alc ctc				
W-->	217 Leu Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu				
218	705	710	715	720	
220	ata tta tac ggg atg agg atg att tca tat tca uaq gct aac atq ctt				2208
221	Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu				
222	725	730	735		2256
224	qaa qct ctg caq qat att gaa att gct tca uaq ata qtt uac ttc qat				
225	Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp				
226	740	745	750		2304
228	age qac aqt gat gaa att ctt qat qat aac tat atq aac att cac ttt				
229	Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys				
230	755	760	765		2352
232	gac atc acc ccg ctg qct cac gat aqt gaa uat lac aqg lha att qaq				
233	Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Ile Glu				
244	770	775	780		2400
236	caq tat ctc aac aca cat gct cct act cac uaq gac tgg tgg ctg				
247	Gln Tyr Leu Leu Asn Thr His Ala Pro Phe His Lys Asp Trp Ser Leu				
238	785	790	795	800	
240	gaa ctg qaq gaa gtt ttt tca ctt qat cqa qar qaa qaa ctt aat aqg				2418
241	Glu Leu Gln Glu Val Phe Ser Leu Asp Arg Asp Gly Gln Leu Asn Lys				
242	805	810	815		2496
244	lac tca aga tat aac aat aat ctg cat aac uaq atq cta tta tgg cac				
245	Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His				
246	820	825	830		2514
248	tgt Lca ugg tlg aeq aat ttt gtg gaa att ctt aqg uaa ggg cta aqa				
249	Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg				
250	835	840	845		2592
252	att uca cct cct qag gca cct qtt act egg tat atq ttc spc aac qgc				
253	Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly				
254	850	855	860		2640
256	ctc lac ttt qca gat cta qta agc aag aqc uaa cua lac tgl tat gta				
257	Leu Dyr Phe Ala Asp Leu Val Ser Lys Ser Ala Cln Tyr Cys Tyr Val				
258	865	870	875	880	
260	qat aqg aat aat cct gta ggt ttg alq ett ett tet gag gtt gct tta				2688
261	Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu				
262	885	890	895		

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Input Set : A:\Polyadpl.app  
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264 gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca	2736
265 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro	
266 900 905 910	
268 aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag	2784
269 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu	
270 915 920 925	
272 tca gaa ttt gtg aag tgg aag gat gat gtc gta gtt ccc tgc ggc aag	2832
273 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys	
274 930 935 940	
276 cgg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac	2880
277 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr	
278 945 950 955 960	
280 atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg	2928
281 Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val	
282 965 970 975	
284 cgt ttc cat cac aag aqq tag	2949
285 Arg Phe His His Lys Arg	
286 980	
289 <210> SEQ ID NO: 2	
290 <211> LENGTH: 982	
291 <212> TYPE: PRT	
292 <213> ORGANISM: Zea mays	
294 <400> SEQUENCE: 2	
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297 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Glu Leu	
298 20 25 30	
299 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro	
300 35 40 45	
301 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Glu Ile Lys	
302 50 55 60	
303 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln	
304 65 70 75 80	
305 Glu Lys Ile Arg Asn Phe Val Gly Ser Ala Ser Ala Gly Thr Ser Ser	
306 85 90 95	
307 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala	
308 100 105 110	
309 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val	
310 115 120 125	
311 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp	
312 130 135 140	
313 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu	
314 145 150 155	160
315 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met	
316 165 170 175	
317 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly	
318 180 185 190	
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320 195 200 205	

See pp 6-7

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6

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see next page

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Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro  
35 40 45  
Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys  
50 55 60  
Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln  
65 70 75 80  
Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser  
85 90 95  
Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala  
100 105 110  
Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val  
115 120 125  
Arg Leu Ser Ala Lys Leu Ser Glu Gly Pro Lys Gly Ile Pro Trp  
130 135 140  
Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu  
145 150 155 160  
Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met  
165 170 175  
Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly  
180 185 190  
Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala  
195 200 205  
Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln  
210 215 220  
Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu  
225 230 235 240  
Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu  
245 250 255  
Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn  
260 265 270  
Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala  
275 280 285  
Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn  
290 295 300  
Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser  
305 310 315 320  
Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys  
325 330 335  
Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys  
340 345 350  
Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro  
355 360 365  
Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu  
370 375 380  
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385 390 395 400  
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405                    410                    415  
Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala  
420                    425                    430  
Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg  
435                    440                    445  
Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys,  
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Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu  
465                    470                    475                    480  
Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala  
485                    490                    495  
Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa  
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Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa  
515                    520                    525  
His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp  
530                    535                    540  
Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser  
545                    550                    555                    560  
Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala  
565                    570                    575  
Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp  
580                    585                    590  
Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe  
595                    600                    605  
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Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu  
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Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu  
645                    650                    655  
Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa  
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675                    680                    685  
Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu  
690                    695                    700  
Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu  
705                    710                    715                    720  
Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu  
725                    730                    735  
Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp  
740                    745                    750  
Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys  
755                    760                    765  
Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu  
770                    775                    780  
Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu  
785                    790                    795                    800  
Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys  
805                    810                    815  
Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His  
820                    825                    830  
Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg  
835                    840                    845  
Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly  
850                    855                    860

all  
item 10  
on Env  
summary  
sheet

VERIFICATION SUMMARY DATE: 11/01/2000  
PATENT APPLICATION: US/09/236,995A TIME: 13:18:35

Input Set : A:\Polyadpl.app  
Output Set: N:\CRF3\11012000\I236995A.raw

L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
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L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:355 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:355 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2  
L:355 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2  
L:355 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:355 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2  
L:357 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:357 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2  
L:357 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2  
L:357 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
M:340 Repeated in SeqNo=2  
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